

ABSTRACT

The present invention provides methods for determining the methylation status of CpG-containing dinucleotides on a genome-wide scale using infrequent cleaving, methylation sensitive restriction endonucleases and two-dimensional gel electrophoretic display of the resulting DNA fragments. Such methods can be used to diagnose cancer, classify tumors and provide prognoses for cancer patients. The present invention also provides isolated polynucleotides and oligonucleotides comprising CpG dinucleotides that are differentially methylated in malignant cells as compared to normal, non-malignant cells. Such polynucleotides and oligonucleotides are useful for diagnosis of cancer. The present invention also provides methods for identifying new DNA clones within a library that contain specific CpG dinucleotides that are differentially methylated in cancer cells as compared to normal cells.